U.S.S.N 09/910,120 Ault-Riche *et al.* PRELIMINARY AMENDMENT ATTACHMENT

MARKED-UP COPY OF FIGURES

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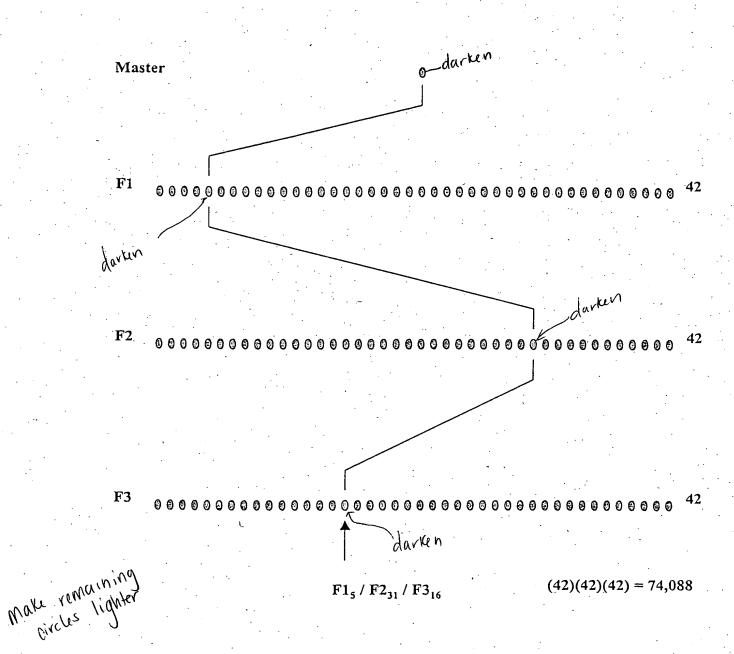
Applicant: Ault-Riche et al. DKT. No. 25885-1751

Priority claimed to 60/219,183

For:COLLECTIONS OF BINDING PROTEINS AND TAGS AND USES THEREOF FOR NESTED SORTING

AND HIGH THROUGHPUT SCREENING

Sorting by pools



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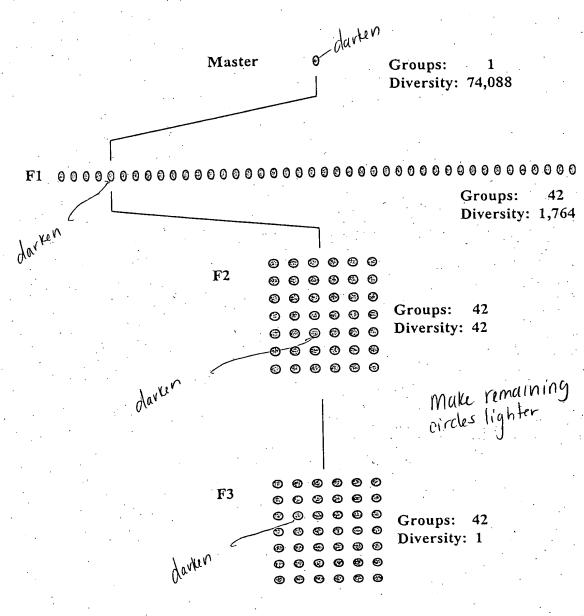
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Sorting by pools: Decreasing pool diversities



F1₅ / F2₃₁ / F3₁₆

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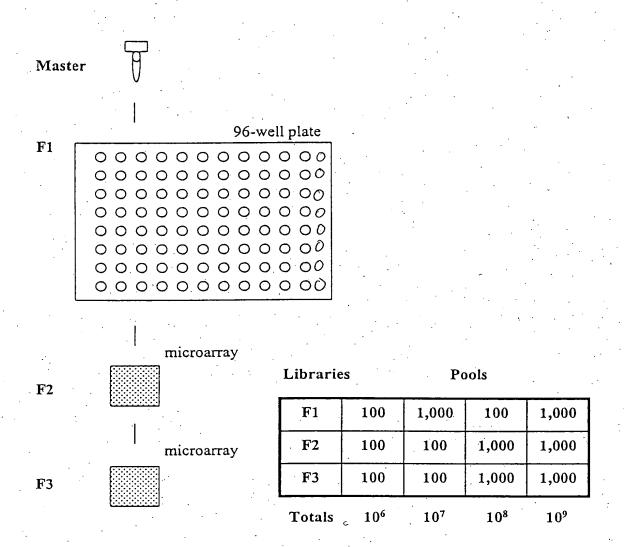
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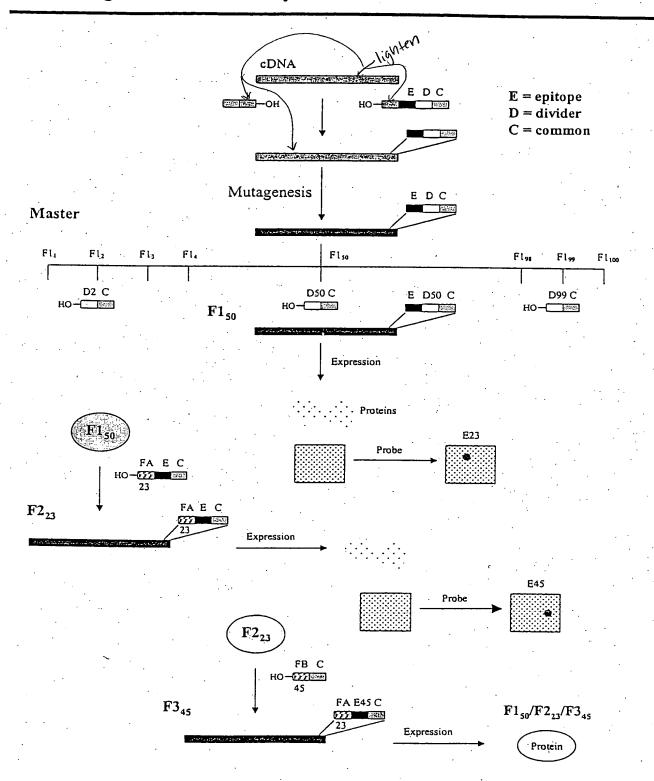
Sorting by pools: Screening large diversity libraries



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Searching a mutation library

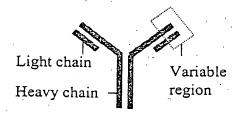


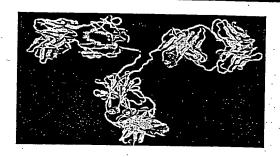
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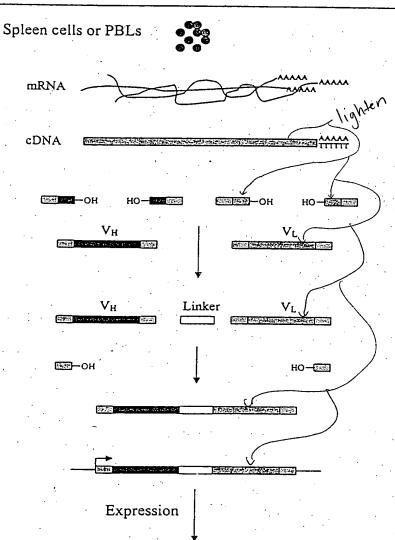
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Making a recombinant antibody library

Basic antibody structure







Antibodies

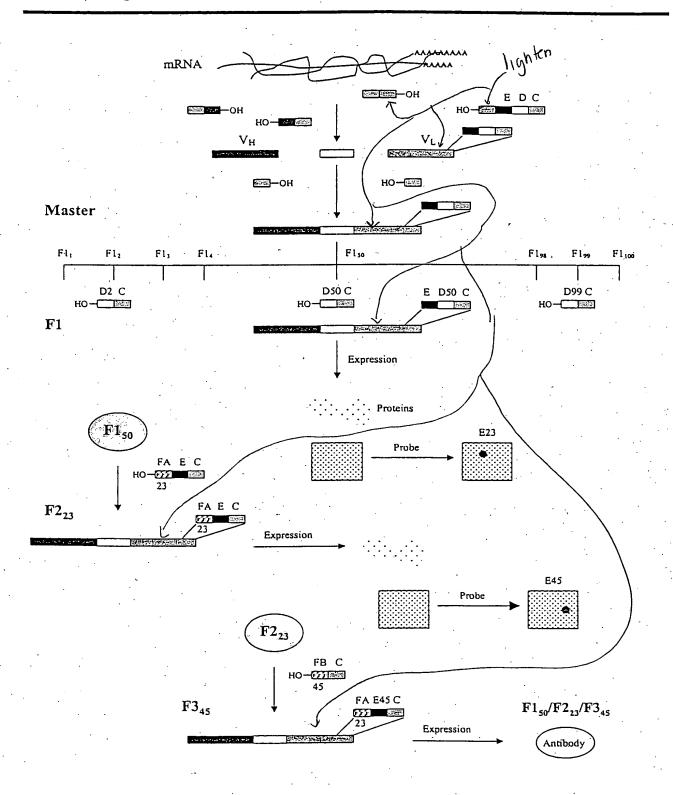
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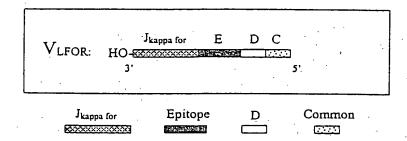
For: COLLECTIONS OF BINDING PROTEINS AND
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Searching a recombinant antibody library

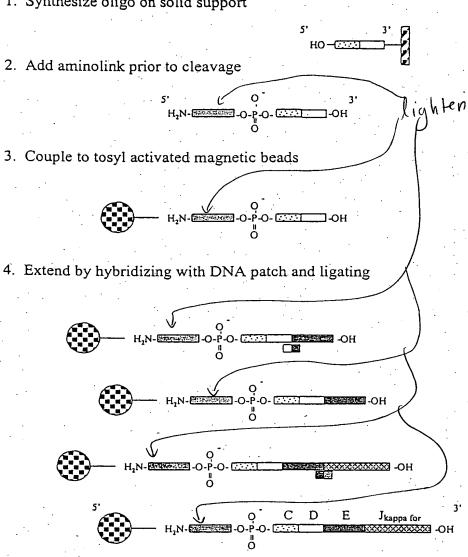


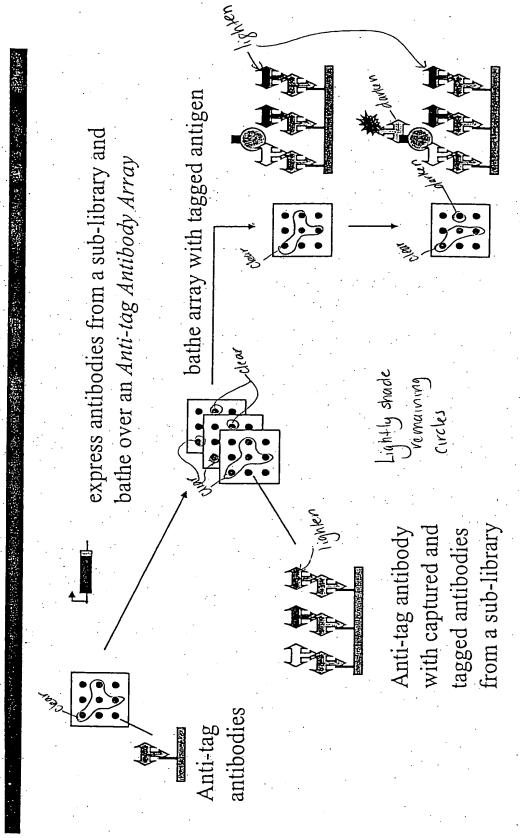
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Making the V_{LFOR} primers: Solid phase synthesis



1. Synthesize oligo on solid support





AND HIGH THROUGHPUT SCREENING

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HELLER EHRMAN WHITE & MCAULIFFE LLP Sheet 16 of 23 ID spot containing the antigen with a labeled developing Ab

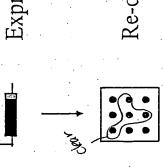
FIGURE 14B

step III

Jourte" Amplify the antibody genes from the identified sub-library using tag-specific PCR primers

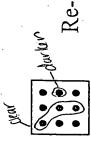
If the starting diversity of the master library was 1,000,000,000 then each spot in this array will have 1,000 different types of rAbs

Express and purify the antibodies



Re-distribute over an Anti-tag Antibody Array

If the starting diversity of the master library was 1,000,000,000 then each spot in this array will have a single type of rAb



Re-survey to ID the antibody of interest

Lightly shade remaining circles

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Clahtly shad	remaining Circles	Aarlen		Clear
	Arrays used		1,000	1
1,000 sub-libraries	Spot diversity		1,000	1
1,000 s	Sub-libraries	1,000		
	Round Library diversity	1,000,000,000	1,000,000	1,000
	Round	0	Н	II

IGURE 14D

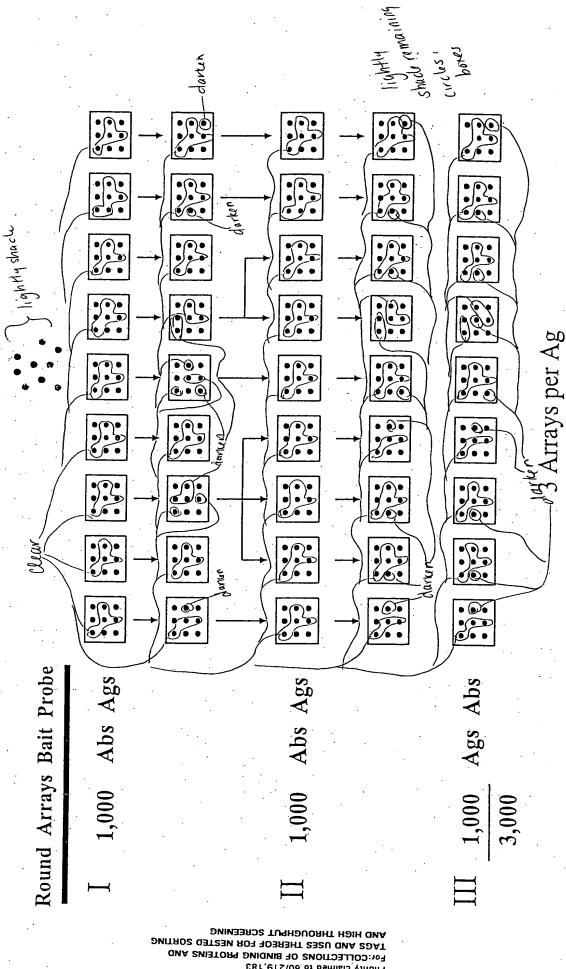
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FIGURE 15

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TAGS AND HIGH THROUGHPUT SCREENING

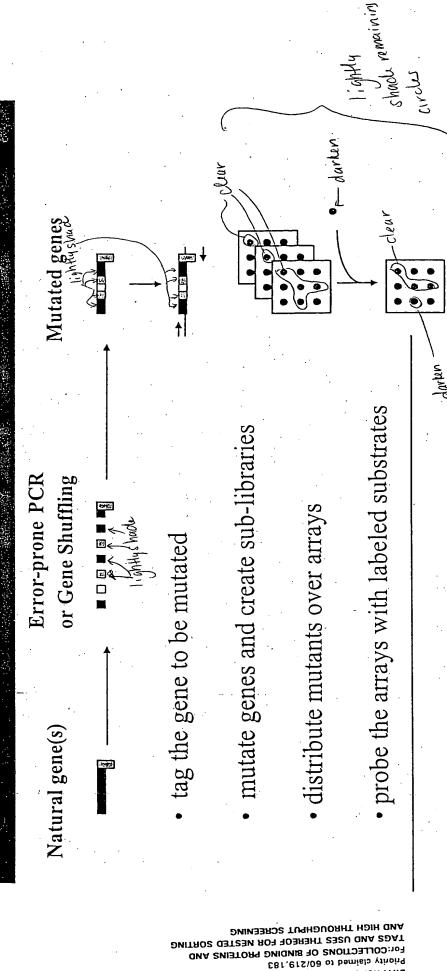
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Simultaneous searches



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Enzyme engineering



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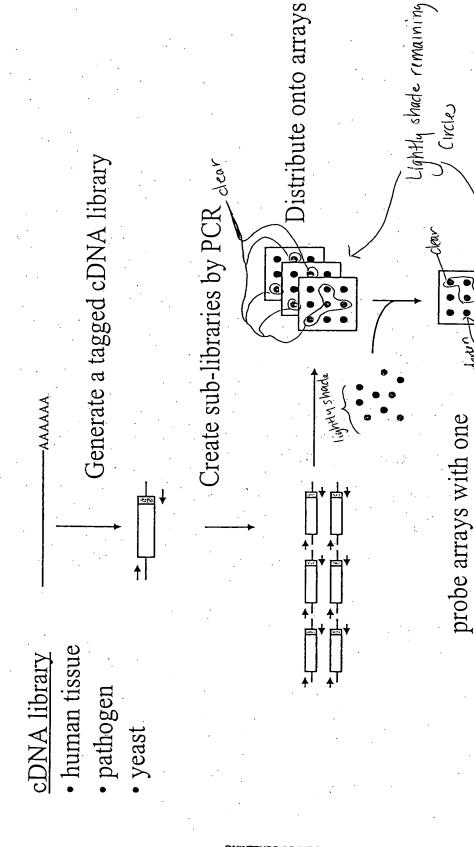
Sheet 21 of 23 неггея енямаи читте & модигіяте сср Spots can contain mixtures of enzymes for detection or pathway engineering

FIGURE 17

or several labeled proteins,

peptides, or drugs

Protein interaction mapping



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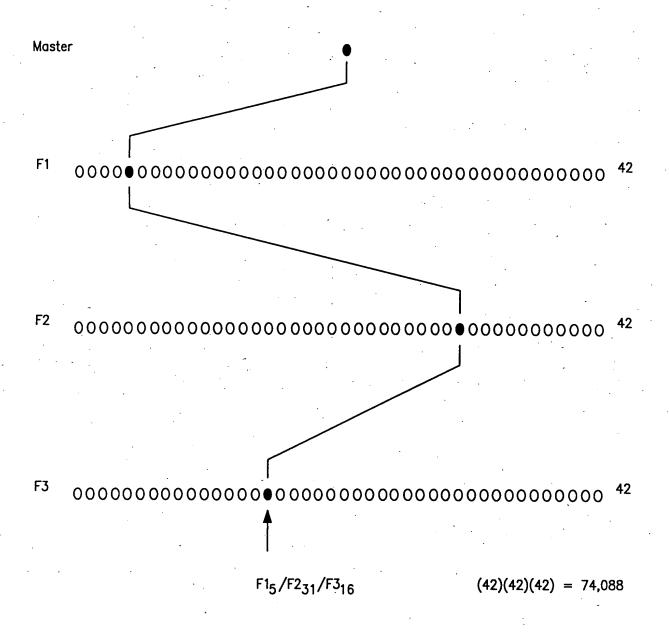


FIG. I

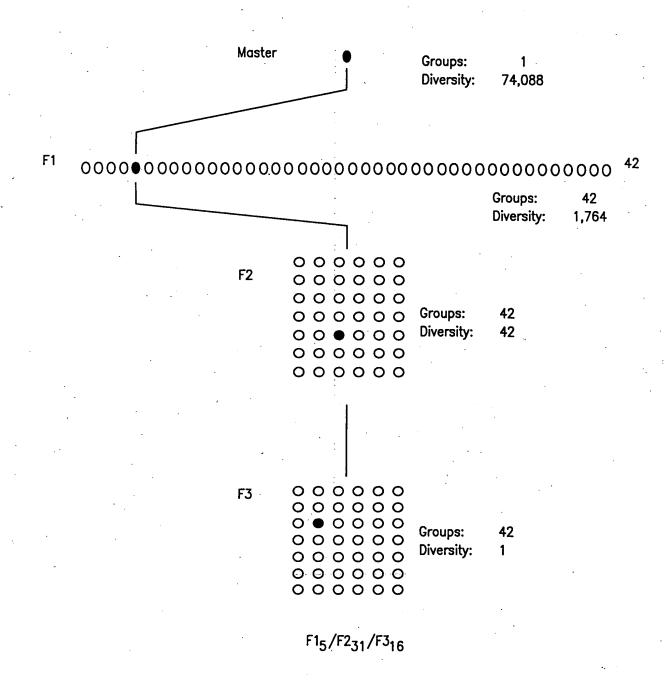


FIG. 2

Sorting by pools: Screening large diversity libraries

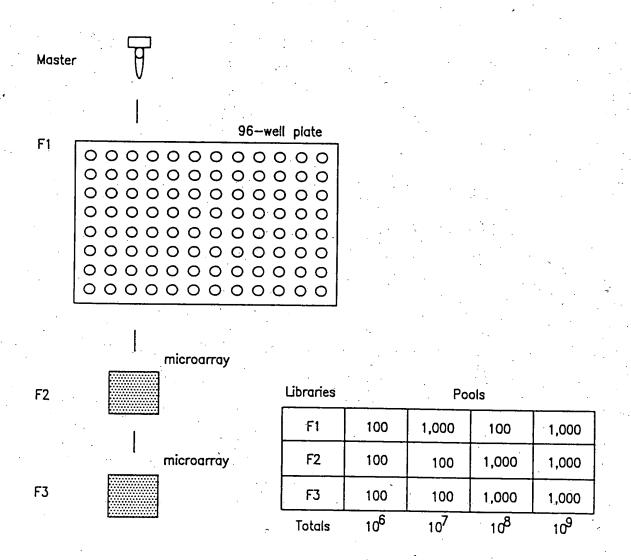


FIG. 3

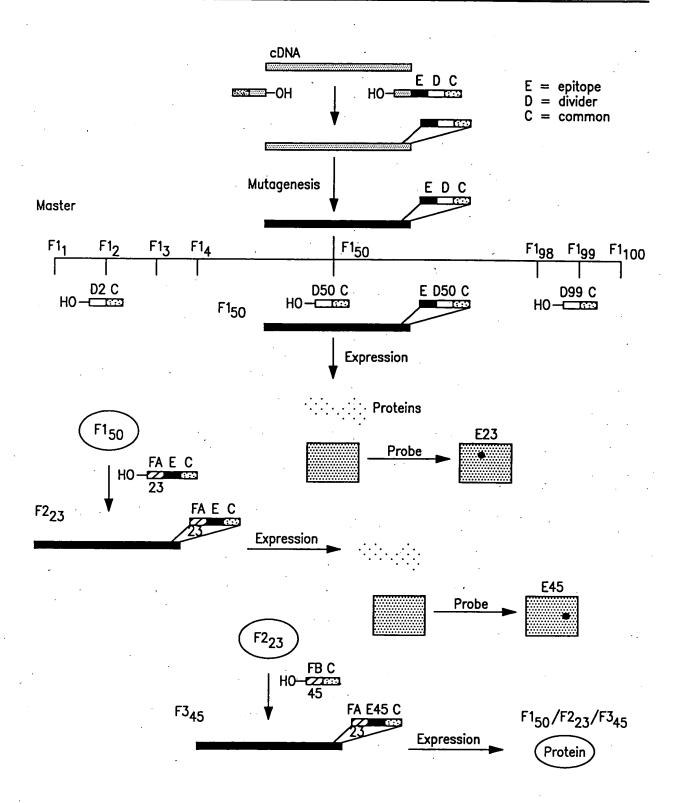
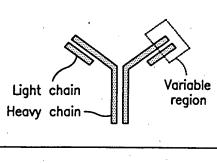
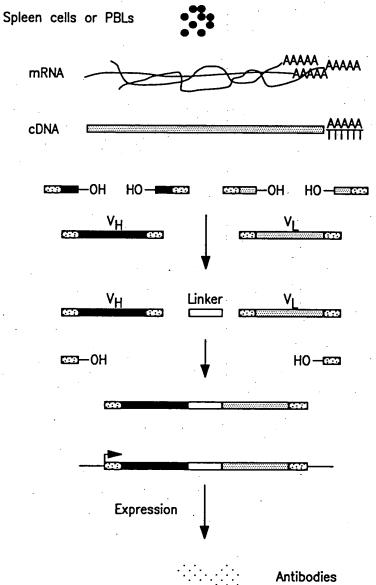


FIG. 4







7 41(15) 0 0100

FIG. 5

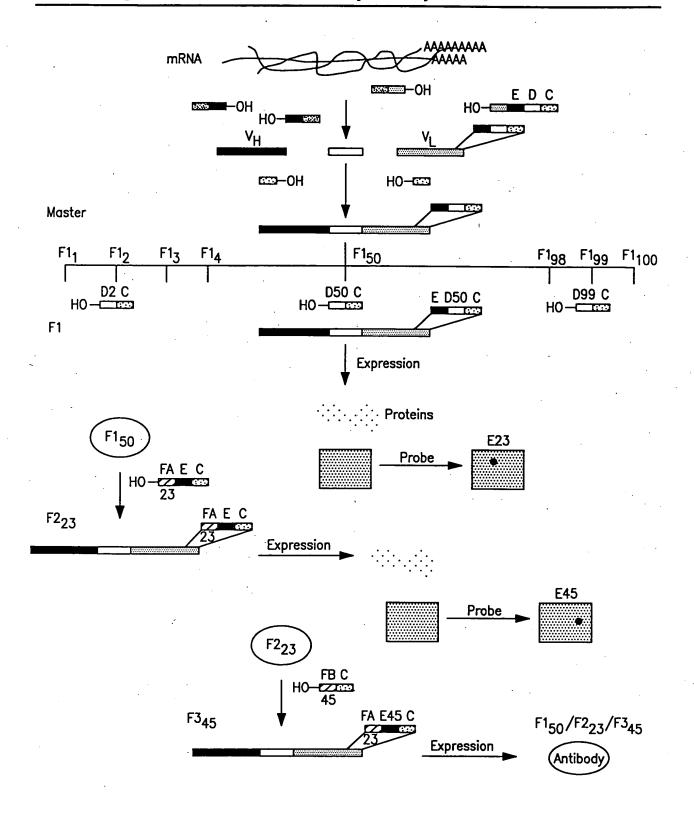
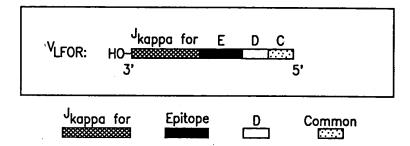


FIG. 8

1

Making the V_{LFOR} primers: Solid phase synthesis



1. Synthesize oligo on solid support

2. Add aminolink prior to cleavage

3. Couple to tosyl activated magnetic beads

4. Extended by hybridizing with DNA patch and ligating

$$H_{2}N - H_{2}N - H$$

FIG. 10

ID spot containing the antigen with a labeled developing Ab

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Amplify the antibody genes from the identified sub-library using tag-specific PCR primers

If the starting diversity of the master library was 1,000,000,000 then each spot in this array will have 1,000 different types of rAbs



Express and purify the antibodies



Re-distribute over an Anti-tag Antibody Array

0 0

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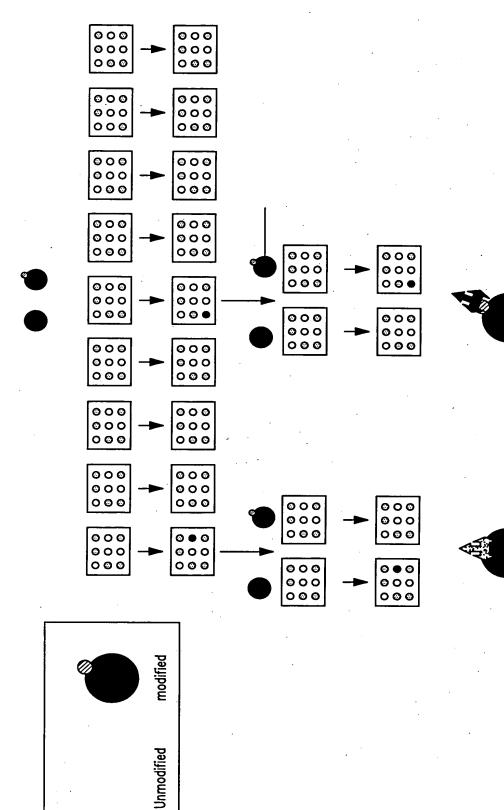
If the starting diversity of the master library was 1,000,000,000 then each spot in this array will have a single type of rAb



Re-survey to ID the antibody of interest

summary

master library

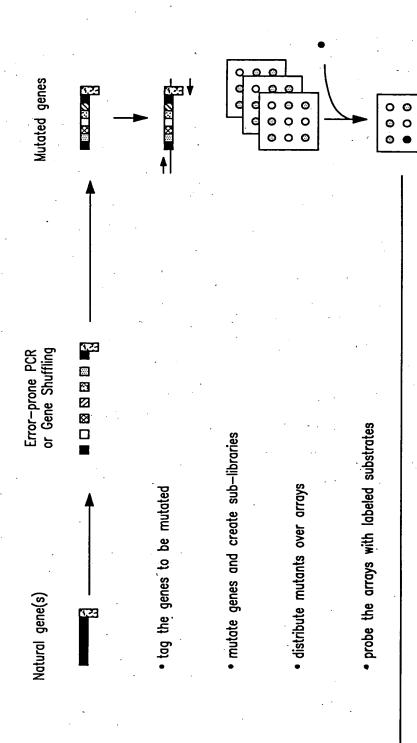


Modification searches

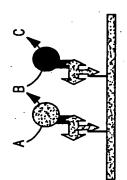
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Simultaneous searches

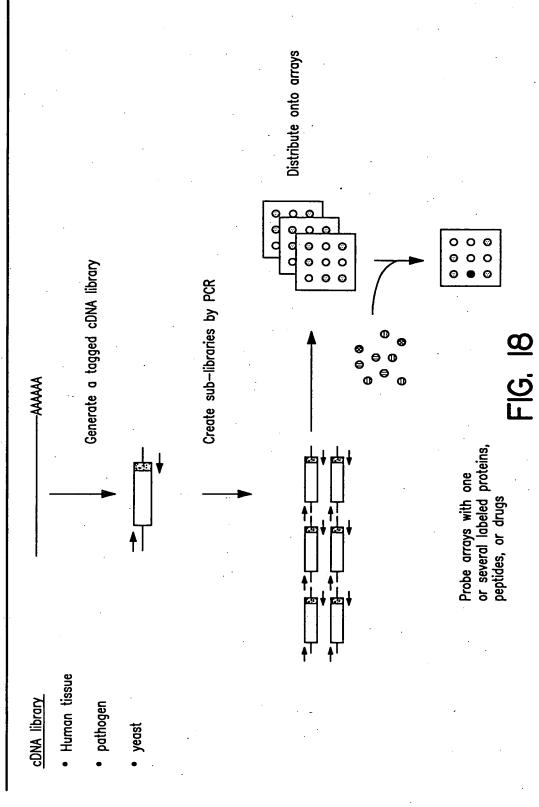
Protein interaction mapping



Spots can contain mixtures of enzymes for detection or pathway engineering



Protein interaction mapping



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